



RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/409,800A
Source: 1645
Date Processed by STIC: 4/25/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/409,800A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 _____ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 _____ Wrapped Aminos The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☒ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 _____ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 _____ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 _____ Variable Length Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 _____ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 8 _____ Skipped Sequences (OLD RULES) Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 _____ Skipped Sequences (NEW RULES) Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 _____ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 _____ Use of "Artificial" (NEW RULES) Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
Valid response is Artificial Sequence.
- 12 _____ Use of <220>Feature (NEW RULES) Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 _____ PatentIn ver. 2.0 "bug" **Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.**

Does Not Comply
Corrected Diskette Needed

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

Blattner,

Frederick R.

Burland, Valerie
 Rose, Debra J.
 Mayhew, George F.
 Perna, Nicole
 Perry, Robert D.
 Straley, Susan C.
 Fetherston, Jacqueline D.
 Lindler, Luther E.
 Plano, Gregory V.

Do NOT use
 TAB codes. They
 do not process well
 in the CRT program

(ii) TITLE OF INVENTION: Plasmid DNA from Yersinia Pestis

(iii) NUMBER OF SEQUENCES: 3

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Quarles & Brady

(B) STREET: 1 South Pinckney

Street

(C) CITY: Madison

(D) STATE: WI

(E) COUNTRY: US

(F) ZIP: 53701-2113

20

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC

compatible

25

(C) OPERATING SYSTEM: PC-

DOS/MS-DOS

(D) SOFTWARE: Word Perfect 8.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

09/409,800

30

(B) FILING DATE: 09/30/99

(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Seay, Nicholas J.

(B) REGISTRATION NUMBER: 27386

(C) REFERENCE/DOCKET NUMBER:

960296.95939

35

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (608) 251-5000

(B) TELEFAX: (608) 251-9166

This page shown as a
sample of global errors

9/409,800A

2

delete

(2) INFORMATION FOR SEQ ID NO: 1

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100990
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (plasmid)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

use upper-case letters

insert

for base when
creating sequence
Listing in "old"

sequence
rules
format

aaacagcccg gcggtgctgga gcgactggaa cgtgaggacg gtgtcattat ccaccagcgt 60
cgcgagtggc gcatgtacga tccggaaaca ggtaagctca cgacgaaggc cggaacgctc 120
tggggtctgc tgaagaaaat ccaactgataa caccaaccac tgcggtgagt agccagctca 180
ccgcgcgcgt atctgggtca taaccactgt agtgagtaaa acggctgccg tggcatccgg 240
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caggcgttca ttcacagcaa acaaccacta tggagagtga tggaaatgcga cctccagcgg 360
gtatccacta tggagagtaa accttcactg ttttcagcgg atgtctactc tccacagtgg 420
atagtaaata cagccaaccg attctgctct ccatagtgga tagccaatag cgaagggagc 480
aacgataacc actatagaga gtggatttaa caagtcaccc agtgaccact aacctcgcag 540
cccttgtttc atctaggttt gtaaccacta acattcattt cgttatttga gcgctactgc 600
ctacagtggc tactattcgg ttgttggttac tcactacagt ggatagcgga cttcagataa 660
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ttgcgagcct ttgccttgcg cagctcttcg agaatcgcca gttcttcctt gctcaacatg 780
accatctcac cgtctttttc ttcaggaaca acatcgatga tgtcctcctg accatcgcca 840
ggcaagttat cttcctgctc ttctggttct tccggcgcag ctttagttgg tggcaatgcc 900
gggcgtaact tccgcccgcct atagtggatg atgaagtaga ccgagctgcc gcgcttcact 960
tcggtgtaat cgagatagcc gatctccgcg agctgctcca tcgccttcct gactgtcgcg 1020
ttctgggtaa tgggtcggct ggtaagtta agtctggcgc gtaagcgagc caacgagatt 1080
ggtgccgggt caggtggcaa actttcgatg aatgtgtaga gtgcctgggc ggattctttt 1140
ctggagagtt cgttgattgc ccggagttgc agaagaacct ttttgcgaa ctggtagagt 1200
tcgaaaatct taggatcagc ctgcagcgag accgtgtcgt tcttagtgct gtactttgct 1260
gtctgcacaa ggtgagttac gtaatactca tcagagcctt tactgcggaa tgagatagtg 1320

lines
exceed

72-character

limit

(see item 3 on Error Summary Sheet)